

SEQUENCE LISTING

<110> Scriptgen
Thompson, M. Craig
Long, Fan
Wobbe, C. Richard

<120> A NOVEL FUNGAL MULTISUBUNIT PROTEIN
COMPLEX CRITICAL FOR EXPRESSION OF FUNGAL PROTEINS

<130> 0342/2D516

<140> Unknown

<141> Filed Concurrently

<150> 60/074,100

<151> 1998-02-09

<160> 32

<170> FastSEQ for Windows Version 3.0

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<211> 4116

<212> DNA

<213> C. albicans

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 <213> C. albicans

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 Ser Asn Asp Phe Asp Ser Asn Ile Ser His His Asp His Met Gly Gly
 65 70 75 80
 Asp Ser Asn Gly Ile Ile Asp Asp Asn His His Ser Ser Val Asn Asp
 85 90 95
 His Asp Gly Leu Phe Asn Asn Leu Gly Asn Gly Asn His Leu Leu Asp
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 Asp Asp Asn Asp Gly Leu Asn Asp Leu Gly Glu Leu Phe Asp Asp Gln
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 Gln Glu Asp Ser Asn Val Ile Asn Thr Lys Lys His Lys Leu Asp Asp
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 Asp Ser Asn Asn Asp Gly Lys Thr Ala Gln Glu Asp Gln Lys Glu Lys
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 Glu Asn Lys Arg Gln Leu Lys Arg Gln Lys Leu Gln Lys Ile Val Lys
 165 170 175
 His Leu Glu Lys Glu Gln Ile Lys Arg Asn Ile Lys Tyr Tyr Phe Pro
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 Thr Tyr Ser Arg His Arg Pro Phe Asn Phe His Lys Phe Phe Ser Pro
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 210 215 220
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 225 230 235 240
 Asp Gln Lys Lys Ile Phe Lys Leu Arg Ser Ala Asp Thr Ala Ser Leu
 245 250 255
 Ser His Glu Asp Lys Asn Val Thr Asn Ile Thr Gln Asp Asp Leu Asp
 260 265 270
 Phe Ile Lys Asn Leu Glu Ser Lys Arg Ser Ser Ile Asp Ser Phe Ile
 275 280 285
 Lys Glu Ile Asp Tyr Val Lys Arg Asp Trp Thr Asn Cys Asp Lys Phe
 290 295 300
 Asp His Tyr Ser Lys Asp Leu Val Leu Ser Thr Thr Asp Trp Asp Asp
 305 310 315 320
 Asp Ala Ile Ile Asn Ala Gly Asp Asn Glu Tyr Ser Ile Val Lys Pro
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 Ile Asn Glu Leu Leu Leu Asn Asn Pro Leu Asp Asn Ser Lys Gln Asn
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Arg Gln Lys Ile Glu Asn Asp Asn Thr Thr Asn Asn Tyr Asn Gln Asn
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 Asn Ser Asn Val Gln Asp Glu Glu Asp Asp Asp Ile Phe Asn Gly
 370 375 380
 Gln Ile Asn Leu Asp Lys Leu Lys Leu Asp Met Asn Asp Pro Asn Leu
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 405 410 415
 Ser Thr Asp Lys Leu Leu Glu Leu Lys Phe Asn Ile Ser Asn Asp Gln
 420 425 430
 Glu Tyr Glu Leu Leu Arg Lys Asn Tyr Asn Thr Lys Gln Arg Ser Gln
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 Leu Ser Asn Leu Asn Ile Glu His Ser Val Pro Ala Leu Arg Leu Gln
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 Thr Pro Tyr Tyr Lys Val Lys Leu Ser Thr Asp Glu Thr Arg Ser Phe
 465 470 475 480
 His Arg Pro Val Phe Asn Val Arg Pro Gly Thr Leu Val Ser Phe Ser
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 Gln Ile Phe Ser Lys Thr Ser Asp Leu Thr Val Ala Asp Thr Gly Asn
 515 520 525
 Ile Ile Ala Leu Glu Tyr Ser Glu Gln Tyr Pro Pro Ile Leu Ser Asn
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 Phe Gly Met Gly Ser Lys Leu Ile Asn Tyr Tyr Arg Lys Glu Arg Pro
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 Gly Val Glu Asp Arg Ser Pro Phe Trp Asn Phe Gly Glu Val Ala Pro
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 Gly Ala Gly Ser His Gln Lys Phe Tyr Leu Arg Gly Ile Asn Phe Asn
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 Phe Ala Val Gly Asn Thr Phe Pro Val Glu Val Pro Ala Pro His Ser
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 Arg Val Met Asn Ser Leu Gly Val Pro Arg Ile Ser Val Lys Asp Val
 675 680 685
 Ser Lys His Phe Pro Glu His Ser Asp Met Gln Asn Arg Gln Arg Leu
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 Lys Val Arg Gly Leu Asn Asp Val Ile Pro Gly Glu Glu Glu Ile Arg
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 Thr Met Ile Thr Pro Glu Asp Ser Ser Leu Met Asp Thr Met Gln Phe
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Gly Gln Gln Val Leu Asp Asp Asn Met Val Leu Phe Gly Glu Gln Ser
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 Arg Gln Glu Ser Ser Arg Ser Arg Lys Gly Asp Lys Arg Glu Asp Ser
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 Ile Gly Leu Gly Phe Ser Met Leu Arg Ala Thr Gln Lys Asn Pro Phe
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 980 985 990
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Asp Asp Asp Asp Asp Leu Pro Glu Glu Ser Asp Ala Asn Leu His Pro
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Val Leu Gly Ile Asp Ser Asn Ser Leu Asn Met Gln Leu Pro Glu Ile
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Asn Gly Asp Leu Ser Gln Gln Phe Ile Leu Glu Asp Asp Gly Gly Thr
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Pro Ala Thr Ser Asn Ala Leu Phe Met Gly Met Asp Ala Asn Glu Ile
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His Leu Ala Thr Glu Thr Gly Val Leu Asp Gly Ser Gly Ala Asn Glu
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Ser Ile Asn Gly Gly Phe Ile Met Glu Pro Asp Met Ser Asp Gly Lys
180 185 190
His Lys Lys Ala Thr Lys Leu Asp Leu Ile Asn His Glu Lys Tyr Leu
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Leu Lys Lys Tyr Phe Pro Asp Phe Glu Lys Gly Lys Ile Leu Lys Trp
210 215 220
Asn Lys Leu Ile Tyr Arg Arg Ser Val Pro Tyr His Trp His Ser Glu
225 230 235 240
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Val Ala Pro Ile Tyr Gln Gly Lys Asn Asn Leu Leu Gln Ser Asn Ser
275 280 285
Ser Ala Ser Arg Arg Gly Leu Ile His Val Ser Ile Asp Glu Leu Phe
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Pro Ile Lys Glu Gln Gln Lys Lys Arg Lys Ile Ile His Asp Glu Lys
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 385 390 395 400
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 Thr Ile Leu Gln Gln Lys Phe Asn Leu Ser Asn Asp Asp Lys Tyr Gln
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 450 455 460
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 Gly Met Ala Asn Lys Leu Ile Asn Tyr Tyr Arg Lys Ala Asn Glu Gln
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 Asp Thr Leu Arg Pro Lys Leu Pro Val Gly Glu Thr His Val Leu Gly
 580 585 590
 Val Gln Asp Lys Ser Pro Phe Trp Asn Phe Gly Phe Val Glu Pro Gly
 595 600 605
 His Ile Val Pro Thr Leu Tyr Asn Asn Met Ile Arg Ala Pro Val Phe
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 Arg Lys Val Thr Ser Met Lys Ala Thr Arg Leu Lys Met Ile Ile Tyr
 675 680 685
 Arg Ile Leu Asn His Asn His Ser Lys Ala Ile Ser Ile Asp Pro Ile
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 Gly Met Ala Ser Arg Ile Val Asn Tyr Tyr Arg Lys Lys Asn Glu Gln
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 Asp Glu Ser Arg Pro Lys Leu Glu Val Gly Glu Ser His Val Leu Asp
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 Val Gln Asp Arg Ser Pro Phe Trp Asn Phe Gly Ser Val Glu Pro Gly
 515 520 525
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 Lys His Glu Val Pro Pro Thr Asp Phe Ile Leu Ile Arg Asn Ser Ser
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 Lys Asp Ala Asp Arg Lys Leu Asp Thr Pro Leu Ala Asp Ile Leu Pro
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 Phe Gly Pro Ala Gln Ile Trp Tyr Asp Ile Leu Glu Val Pro Asp Ser
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 Gly Glu Gly Phe Asn Tyr Gly Phe Lys Thr Lys Ala Ala Ser Thr Ser
 370 375 380
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 385 390 395 400
 Asp Val Glu Asp Pro Ser Ile Ala Asp Asp Ala Phe Leu Met Val Ser
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 420 425 430
 Ala Lys Val Leu Gln Lys Leu Asn Ser Lys Thr Asn Ala Ala Gly Trp
 435 440 445
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 450 455 460
 Lys Pro Ser Met Pro Val Gly Ser Gly Ser Ser Lys Gln Gly Ser Gly
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 Val Val Glu Leu Arg Ala Pro Phe Val Pro Thr His Met Gly Pro Met
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 Asn Val Arg Ala Phe His Arg Pro Pro Leu Lys Lys Tyr Ser His Gly
 660 665 670
 Pro Met Ala Gln Ser Ile Pro His Pro Val Phe Pro Leu Leu Lys Thr
 675 680 685
 Ile Ala Lys Lys Ala Lys Gln Arg Glu Val Glu Arg Ile Ala Ser Gly
 690 695 700
 Gly Gly Asp Val Phe Phe Met Arg Asn Pro Glu Asp Leu Ser Gly Arg
 705 710 715 720
 Asp Gly Asp Ile Val Leu Ala Glu Phe Cys Glu Glu His Pro Pro Leu
 725 730 735
 Ile Asn Gln Val Gly Met Cys Ser Lys Ile Lys Asn Tyr Tyr Lys Arg
 740 745 750
 Lys Ala Glu Lys Asp Ser Gly Pro Gln Asp Tyr Val Tyr Gly Glu Val
 755 760 765
 Ala Phe Ala His Thr Ser Pro Phe Leu Gly Ile Leu His Pro Gly Gln
 770 775 780
 Cys Ile Gln Ala Ile Glu Asn Asn Met Tyr Arg Ala Pro Ile Tyr Pro
 785 790 795 800
 His Lys Met Ala His Asn Asp Phe Leu Val Ile Arg Thr Arg Asn Asn
 805 810 815
 Tyr Trp Ile Arg Ser Val Asn Ser Ile Tyr Thr Val Gly Gln Glu Cys
 820 825 830
 Pro Leu Tyr Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn Asn Phe
 835 840 845
 Thr Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp Lys Ser
 850 855 860
 Arg Asp Asn Pro Arg Arg Ile Arg Met Asp Asp Ile Lys Gln Ala Phe
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 Pro Ala His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Gln Cys Ala
 885 890 895
 Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Ile Lys Pro
 900 905 910
 Glu Phe Arg Leu Pro Ser Glu Glu Glu Ile Arg Ala Met Val Ser Pro
 915 920 925
 Glu Gln Cys Cys Ala Tyr Phe Ser Met Ile Ala Ala Glu Gln Arg Leu
 930 935 940
 Lys Asp Ala Gly Tyr Gly Glu Lys Phe Leu Phe Ala Pro Gln Glu Asp

09601962 100000

1345 1350 1355 136
 Asn Lys Ala Cys Pro Leu Tyr Ser Gly Met Gln Ser Ser Leu Ser Gln
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 Ser Asn Pro Ser Leu Ala Asp Asp Phe Asp Glu Gln Ser Glu Lys Glu
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 Met Thr Met Asp Asp Asp Asp Leu Val Asn Val Asp Gly Thr Lys Val
 1395 1400 1405
 Thr Leu Ser Ser Lys Ile Leu Lys Arg His Gly Gly Asp Asp Gly Lys
 1410 1415 1420
 Arg Arg Ser Gly Ser Ser Ser Gly Phe Thr Leu Lys Val Pro Arg Asp
 1425 1430 1435 144
 Ala Met Gly Lys Lys Lys Arg Arg Val Gly Gly Asp Leu His Cys Asp
 1445 1450 1455
 Tyr Leu Gln Arg His Asn Lys Thr Ala Asn Arg Arg Arg Thr Asp Pro
 1460 1465 1470
 Val Val Val Leu Ser Ser Ile Leu Glu Ile Ile His Asn Glu Leu Arg
 1475 1480 1485
 Ser Met Pro Asp Val Ser Pro Phe Leu Phe Pro Val Ser Ala Lys Lys
 1490 1495 1500
 Val Pro Asp Tyr Tyr Arg Val Val Thr Lys Pro Met Asp Leu Gln Thr
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 1525 1530 1535
 Leu Glu Asp Leu Lys Gln Ile Val Asp Asn Ser Leu Ile Tyr Asn Gly
 1540 1545 1550
 Pro Gln Ser Ala Tyr Thr Leu Ala Ala Gln Arg Met Phe Ser Ser Cys
 1555 1560 1565
 Phe Glu Leu Leu Ala Glu Arg Glu Asp Lys Leu Met Arg Leu Glu Lys
 1570 1575 1580
 Ala Ile Asn Pro Leu Leu Asp Asp Asp Asp Gln Val Ala Leu Ser Phe
 1585 1590 1595 160
 Ile Phe Asp Lys Leu His Ser Gln Ile Lys Gln Leu Pro Glu Ser Trp
 1605 1610 1615
 Pro Phe Leu Lys Pro Val Asn Lys Lys Gln Val Lys Asp Tyr Tyr Thr
 1620 1625 1630
 Val Ile Lys Arg Pro Met Asp Leu Glu Thr Ile Gly Lys Asn Ile Glu
 1635 1640 1645
 Ala His Arg Tyr His Ser Arg Ala Glu Tyr Leu Ala Asp Ile Glu Leu
 1650 1655 1660
 Ile Ala Thr Asn Cys Glu Gln Tyr Asn Gly Ser Asp Thr Arg Tyr Thr
 1665 1670 1675 168
 Lys Phe Ser Lys Lys Ile Leu Glu Tyr Ala Gln Thr Gln Leu Ile Glu
 1685 1690 1695
 Phe Ser Glu His Cys Gly Gln Leu Glu Asn Asn Ile Ala Lys Thr Gln
 1700 1705 1710
 Glu Arg Ala Arg Glu Asn Ala Pro Glu Phe Asp Glu Ala Trp Gly Asn
 1715 1720 1725
 Asp Asp Tyr Asn Phe Asp Arg Gly Ser Arg Ala Ser Ser Pro Gly Asp
 1730 1735 1740
 Asp Tyr Ile Asp Val Glu Gly His Gly Gly His Ala Ser Ser Ser Asn

Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr
1 5 10 15

Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
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 Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
 35 40 45
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 His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
 65 70 75 80
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 85 90 95
 Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
 100 105 110
 Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
 115 120 125
 Gly Ser Leu Gln Pro Leu Cys His Ser Asp Tyr Asp Glu Asp Asp Tyr
 130 135 140
 Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
 145 150 155 160
 Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
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 Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
 180 185 190
 Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
 195 200 205
 Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
 210 215 220
 Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
 225 230 235 240
 Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
 245 250 255
 Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
 260 265 270
 Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
 275 280 285
 Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
 290 295 300
 Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
 305 310 315 320
 Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
 325 330 335
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 Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
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 370 375 380
 Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
 385 390 395 400
 Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
 405 410 415

Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
 420 425 430
 Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
 435 440 445
 Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
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 Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
 465 470 475 480
 Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu
 485 490 495
 Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
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 Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
 515 520 525
 Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
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 Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
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 Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
 565 570 575
 Gln Gln Gly Leu Arg Gly Thr Phe Gly Asn Ile Ile Gln His Ser
 580 585 590
 Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met Gly
 595 600 605
 Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
 610 615 620
 Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
 625 630 635 640
 Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
 645 650 655
 Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
 660 665 670
 Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
 675 680 685
 Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
 690 695 700
 Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
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 Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
 725 730 735
 Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
 740 745 750
 Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
 755 760 765
 Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln
 770 775 780
 Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
 785 790 795 800
 Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
 805 810 815

Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
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 Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
 835 840 845
 Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
 850 855 860
 Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
 865 870 875 880
 Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
 885 890 895
 Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
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 Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
 915 920 925
 Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
 930 935 940
 Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
 945 950 955 960
 Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
 965 970 975
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 980 985 990
 Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
 995 1000 1005
 Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp Glu
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 Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg Ser Gly
 1025 1030 1035 104
 Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe Ser Val Ala
 1045 1050 1055
 Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg Ile Phe Asp Leu
 1060 1065 1070
 Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu Ser Thr Asp Thr Asp
 1075 1080 1085
 Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu Glu Met Gly Lys Asn Ile
 1090 1095 1100
 Glu Asn Met Leu Gln Asn Lys Lys Thr Ser Ser Gln Leu Ser Arg Glu
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 Arg Glu Glu Gln Glu Arg Lys Glu Leu Gln Arg Met Leu Leu Ala Ala
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 Gly Ser Ala Ala Ser Gly Asn Asn His Arg Asp Asp Asp Thr Ala Ser
 1140 1145 1150
 Val Thr Ser Leu Asn Ser Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr
 1155 1160 1165
 Arg Thr Phe Arg Asp Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr
 1170 1175 1180
 Val Arg Lys Pro Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr
 1185 1190 1195 120
 Lys Asp Glu Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His
 1205 1210 1215

Arg Glu Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Gly Gln Leu Arg
 1220 1225 1230
 Arg Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
 1235 1240 1245
 Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys Cys
 1250 1255 1260
 Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe Cys Pro
 1265 1270 1275 128
 Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val Ala Met Thr
 1285 1290 1295
 Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile His Asn Asp Asn
 1300 1305 1310
 Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile Val Leu Gly Lys Gln
 1315 1320 1325
 Leu Ile Glu Ser Ala Asp Glu Val Arg Arg Lys Ser Leu Val Leu Lys
 1330 1335 1340
 Phe Pro Lys Gln Gln Leu Pro Pro Lys Lys Lys Arg Arg Val Gly Thr
 1345 1350 1355 136
 Thr Val His Cys Asp Tyr Leu Asn Arg Pro His Lys Ser Ile His Arg
 1365 1370 1375
 Arg Arg Thr Asp Pro Met Val Thr Leu Ser Ser Ile Leu Glu Ser Ile
 1380 1385 1390
 Ile Asn Asp Met Arg Asp Leu Pro Asn Thr Tyr Pro Phe His Thr Pro
 1395 1400 1405
 Val Asn Ala Lys Val Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro
 1410 1415 1420
 Met Asp Leu Gln Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro
 1425 1430 1435 144
 Ser Arg Glu Glu Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn Ser
 1445 1450 1455
 Ala Thr Tyr Asn Gly Pro Lys His Ser Leu Thr Gln Ile Ser Gln Ser
 1460 1465 1470
 Met Leu Asp Leu Cys Asp Glu Lys Leu Lys Glu Lys Glu Asp Lys Leu
 1475 1480 1485
 Ala Arg Leu Glu Lys Ala Ile Asn Pro Leu Leu Asp Asp Asp Asp Gln
 1490 1495 1500
 Val Ala Phe Ser Phe Ile Leu Asp Asn Ile Val Thr Gln Lys Met Met
 1505 1510 1515 152
 Ala Val Pro Asp Ser Trp Pro Phe His His Pro Val Asn Lys Lys Phe
 1525 1530 1535
 Val Pro Asp Tyr Tyr Lys Val Ile Val Asn Pro Met Asp Leu Glu Thr
 1540 1545 1550
 Ile Arg Lys Asn Ile Ser Lys His Lys Tyr Gln Ser Arg Glu Ser Phe
 1555 1560 1565
 Leu Asp Asp Val Asn Leu Ile Leu Ala Asn Ser Val Lys Tyr Asn Gly
 1570 1575 1580
 Pro Glu Ser Gln Tyr Thr Lys Thr Ala Gln Glu Ile Val Asn Val Cys
 1585 1590 1595 160
 Tyr Gln Thr Leu Thr Glu Tyr Asp Glu His Leu Thr Gln Leu Glu Lys
 1605 1610 1615

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<210> 7
<211> 429
<212> PRT
<213> C. albicans
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Asn	Val	Gln	Asp	Glu	Glu	Glu	Asp	Asp	Asp	Ile	Phe	Asn	Gly	Gln	Ile
		35					40					45			
Asn	Leu	Asp	Lys	Leu	Lys	Leu	Asp	Met	Asn	Asp	Pro	Asn	Leu	Leu	Phe
	50					55					60				
Val	Pro	Ser	Lys	Lys	Val	Asp	Ala	Thr	Lys	Ser	Val	Val	Pro	Ser	Thr
65					70					75					80
Asp	Lys	Leu	Leu	Glu	Leu	Lys	Phe	Asn	Ile	Ser	Asn	Asp	Gln	Glu	Tyr

85 90 95
 Glu Leu Leu Arg Lys Asn Tyr Asn Thr Lys Gln Arg Ser Gln Leu Ser
 100 105 110
 Asn Leu Asn Ile Glu His Ser Val Pro Ala Leu Arg Leu Gln Thr Pro
 115 120 125
 Tyr Tyr Lys Val Lys Leu Ser Thr Asp Glu Thr Arg Ser Phe His Arg
 130 135 140
 Pro Val Phe Asn Val Arg Pro Gly Thr Leu Val Ser Phe Ser Lys Leu
 145 150 155 160
 Lys Leu Arg Lys Arg Lys Lys Asp Lys Gly Lys Ser Leu Gln Gln Ile
 165 170 175
 Phe Ser Lys Thr Ser Asp Leu Thr Val Ala Asp Thr Gly Asn Ile Ile
 180 185 190
 Ala Leu Glu Tyr Ser Glu Gln Tyr Pro Pro Ile Leu Ser Asn Phe Gly
 195 200 205
 Met Gly Ser Lys Leu Ile Asn Tyr Tyr Arg Lys Glu Arg Pro Asn Asp
 210 215 220
 Thr Ser Arg Pro Lys Ala Gln Ile Gly Glu Thr His Ile Leu Gly Val
 225 230 235 240
 Glu Asp Arg Ser Pro Phe Trp Asn Phe Gly Glu Val Ala Pro Gly Asp
 245 250 255
 Phe Val Pro Thr Leu Tyr Asn Asn Met Val Arg Ala Pro Ile Phe Lys
 260 265 270
 His Asp Asn Lys Pro Thr Asp Phe Leu Leu Val Lys Ser Gln Gly Ala
 275 280 285
 Gly Ser His Gln Lys Phe Tyr Leu Arg Gly Ile Asn Phe Asn Phe Ala
 290 295 300
 Val Gly Asn Thr Phe Pro Val Glu Val Pro Ala Pro His Ser Arg Lys
 305 310 315 320
 Val Thr Asn Ile Ser Lys Asn Arg Leu Lys Met Val Val Phe Arg Val
 325 330 335
 Met Asn Ser Leu Gly Val Pro Arg Ile Ser Val Lys Asp Val Ser Lys
 340 345 350
 His Phe Pro Glu His Ser Asp Met Gln Asn Arg Gln Arg Leu Lys Glu
 355 360 365
 Phe Met Glu Tyr Gln Arg Gln Gly Glu Asp Gln Gly Tyr Trp Lys Val
 370 375 380
 Arg Gly Leu Asn Asp Val Ile Pro Gly Glu Glu Glu Ile Arg Thr Met
 385 390 395 400
 Ile Thr Pro Glu Asp Ser Ser Leu Met Asp Thr Met Gln Phe Gly Gln
 405 410 415
 Gln Val Leu Asp Asp Asn Met Val Leu Phe Gly Glu Gln
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<211> 434

<212> PRT

<213> S. cerevisiae

<400> 8

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 Asp Ala Lys Leu Lys Glu Ser Lys His Ala Glu Leu Asn Met Asn Asp
 35 40 45
 Glu Lys Leu Leu Leu Met Ile Glu Lys Thr Asn Asn Leu Ala Gln Gln
 50 55 60
 Lys Gln Gln Leu Asp Ser Ser Asn Leu Ile Leu Pro Leu Asn Glu Thr
 65 70 75 80
 Ile Leu Gln Gln Lys Phe Asn Leu Ser Asn Asp Asp Lys Tyr Gln Ile
 85 90 95
 Leu Lys Lys Thr His Gln Thr Lys Val Arg Ser Thr Ile Ser Asn Leu
 100 105 110
 Asn Ile Gln His Ser Gln Pro Ala Ile Asn Leu Gln Ser Pro Phe Tyr
 115 120 125
 Lys Val Ala Val Pro Arg Tyr Gln Leu Arg His Phe His Arg Glu Asn
 130 135 140
 Phe Gly Ser His Ile Arg Pro Gly Thr Lys Ile Val Phe Ser Lys Leu
 145 150 155 160
 Lys Ala Arg Lys Arg Lys Arg Asp Lys Gly Lys Asp Val Lys Glu Ser
 165 170 175
 Phe Ser Thr Ser Gln Asp Leu Thr Ile Gly Asp Thr Ala Pro Val Tyr
 180 185 190
 Leu Met Glu Tyr Ser Glu Gln Thr Pro Val Ala Leu Ser Lys Phe Gly
 195 200 205
 Met Ala Asn Lys Leu Ile Asn Tyr Tyr Arg Lys Ala Asn Glu Gln Asp
 210 215 220
 Thr Leu Arg Pro Lys Leu Pro Val Gly Glu Thr His Val Leu Gly Val
 225 230 235 240
 Gln Asp Lys Ser Pro Phe Trp Asn Phe Gly Phe Val Glu Pro Gly His
 245 250 255
 Ile Val Pro Thr Leu Tyr Asn Asn Met Ile Arg Ala Pro Val Phe Lys
 260 265 270
 His Asp Ile Ser Gly Thr Asp Phe Leu Leu Thr Lys Ser Ser Gly Phe
 275 280 285
 Gly Ile Ser Asn Arg Phe Tyr Leu Arg Asn Ile Asn His Leu Phe Thr
 290 295 300
 Val Gly Gln Thr Phe Pro Val Glu Glu Ile Pro Gly Pro Asn Ser Arg
 305 310 315 320
 Lys Val Thr Ser Met Lys Ala Thr Arg Leu Lys Met Ile Ile Tyr Arg
 325 330 335
 Ile Leu Asn His Asn His Ser Lys Ala Ile Ser Ile Asp Pro Ile Ala
 340 345 350
 Lys His Phe Pro Asp Gln Asp Tyr Gly Gln Asn Arg Gln Lys Val Lys
 355 360 365
 Glu Phe Met Lys Tyr Gln Arg Asp Gly Pro Glu Lys Gly Leu Trp Arg
 370 375 380
 Leu Lys Asp Asp Glu Lys Leu Leu Asp Asn Glu Ala Val Lys Ser Leu
 385 390 395 400

Ile Thr Pro Glu Gln Ile Ser Gln Val Glu Ser Met Ser Gln Gly Leu
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 Gln Phe Gln Glu Asp Asn Glu Ala Tyr Asn Phe Asp Ser Lys Leu Lys
 420 425 430
 Ser Leu

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 <212> PRT
 <213> S. pombe

<400> 9

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 Thr Ser Lys Val Val Leu Asn Leu Asn Asp Pro Lys Leu Leu Gln
 35 40 45
 Pro Gln Leu Pro Lys Lys Glu Asp Ser Gln Arg Ser Phe Ala Asp Thr
 50 55 60
 His Gln Arg Asn Ser Leu Ala Trp Lys Phe Asn Ile Ser Asn Asp Pro
 65 70 75 80
 Ala Tyr Glu Met Leu Lys Gln Asn His Gln Ser Lys Val Arg Asn Thr
 85 90 95
 Leu Ser Gln Leu Ala Ile Glu His Ala Phe Ala Glu Lys Leu Thr
 100 105 110
 Phe Pro Tyr Tyr Lys Thr Arg Leu Ser Lys Arg Ala Val Arg Ser Tyr
 115 120 125
 His Arg Pro Thr Met Ser Phe Lys Pro Asn Ala Ala Ile Val Phe Ser
 130 135 140
 Pro Leu Ile Val Arg Lys Arg Ser Lys Asp Lys His Lys Ser Glu Arg
 145 150 155 160
 Glu Leu Ile Pro Thr Thr Lys Glu Ile Thr Met Gly Asp Thr Thr His
 165 170 175
 Ala Ile Leu Val Glu Phe Ser Glu Glu His Pro Ala Val Leu Ser Asn
 180 185 190
 Ala Gly Met Ala Ser Arg Ile Val Asn Tyr Tyr Arg Lys Lys Asn Glu
 195 200 205
 Gln Asp Glu Ser Arg Pro Lys Leu Glu Val Gly Glu Ser His Val Leu
 210 215 220
 Asp Val Gln Asp Arg Ser Pro Phe Trp Asn Phe Gly Ser Val Glu Pro
 225 230 235 240
 Gly Glu Ile Thr Pro Thr Leu Tyr Asn Lys Met Ile Arg Ala Pro Leu
 245 250 255
 Phe Lys His Glu Val Pro Pro Thr Asp Phe Ile Leu Ile Arg Asn Ser
 260 265 270
 Ser Ser Tyr Gly Ser Lys Tyr Tyr Leu Lys Asn Ile Asn His Met Phe
 275 280 285
 Val Ser Gly Gln Thr Phe Pro Val Thr Asp Val Pro Gly Pro His Ser

290 295 300
 Arg Lys Val Thr Thr Ala Ser Lys Asn Arg Leu Lys Met Leu Val Phe
 305 310 315 320
 Arg Leu Ile Arg Arg Ser Pro Asn Gly Gly Leu Phe Ile Arg Gln Leu
 325 330 335
 Ser Lys His Phe Ser Asp Gln Asn Glu Met Gln Ile Arg Gln Arg Leu
 340 345 350
 Lys Glu Phe Met Glu Tyr Lys Lys Lys Gly Asp Gly Pro Gly Tyr Trp
 355 360 365
 Lys Leu Lys Ser Asn Glu Val Val Pro Asp Glu Ala Gly Thr Arg Ser
 370 375 380
 Met Val Ser Pro Glu Thr Val Cys Leu Leu Glu Ser Met Gln Val Gly
 385 390 395 400
 Val Arg Gln Leu Glu Asp Ala Gly Tyr Gly Lys Thr Met Asp Glu
 405 410 415

<210> 10

<211> 481

<212> PRT

<213> Human

<400> 10

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 Trp Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg
 35 40 45
 Trp Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu
 50 55 60
 Glu Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu
 65 70 75 80
 Glu Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys
 85 90 95
 Glu Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly
 100 105 110
 Lys Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro
 115 120 125
 Glu Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro
 130 135 140
 Lys Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His
 145 150 155 160
 Ser Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met
 165 170 175
 Gly Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr
 180 185 190
 Ser Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu
 195 200 205
 Leu Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln
 210 215 220

Ala Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu
 225 230 235 240
 Thr Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn
 245 250 255
 Gly Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr
 260 265 270
 Tyr Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr
 275 280 285
 Gly Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His
 290 295 300
 Pro Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro
 305 310 315 320
 Ile Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr
 325 330 335
 Arg Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly
 340 345 350
 Gln Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala
 355 360 365
 Asn Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe
 370 375 380
 Trp Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys
 385 390 395 400
 Lys Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys
 405 410 415
 Leu Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val
 420 425 430
 Leu Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met
 435 440 445
 Val Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu
 450 455 460
 Gln Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro
 465 470 475 480
 Glu

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 <213> C. albicans

<400> 11
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 Glu Lys Glu Lys Glu Gln Glu Arg Glu Glu Glu Lys Gly Lys Asp Lys
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 Glu Lys Asp Lys Asp Lys Glu Lys Asp Lys Thr Glu Lys Glu Lys Ser
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 Lys Lys Ser Lys Glu Gln Asp Thr Glu Ile Asp Val Glu Glu Glu Leu
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 Ala Pro Trp Asn Leu Ser Arg Asn Phe Val

65

70

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<213> "Artificial Sequence"

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<223> Inosine

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18

<210> 13
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<212> DNA
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<400> 13
gayccwachg gwtgtggwga agg

23

<210> 14
<211> 24
<212> DNA
<213> "Artificial Sequence"

<400> 14
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24

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<223> Inosine

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19

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<213> "Artificial Sequence"

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30

<210> 17
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 <212> DNA
 <213> "Artificial Sequence"

<400> 17
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29

<210> 18
 <211> 37
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 <213> "Artificial Sequence"

<400> 18
 ggaattccat atgcttttgc tcaacaatcc cttggac

37

<210> 19
 <211> 32
 <212> DNA
 <213> "Artificial Sequence"

<400> 19
 cgcggtatccc tgctctgctc accgaataac ac

32

<210> 20
 <211> 37
 <212> DNA
 <213> "Artificial Sequence"

<400> 20
 ggaattccat atgagcctgg caggctggct tccttct

37

<210> 21
 <211> 33
 <212> DNA
 <213> "Artificial Sequence"

<400> 21
 ccgctcgagt tctggagcaa aaaaggattt ctc

33

<210> 22
 <211> 0
 <212> DNA
 <213> Human

<400> 22
 Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr
 1 5 10 15
 Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
 20 25 30

Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
 35 40 45
 Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
 50 55 60
 His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
 65 70 75 80
 Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
 85 90 95
 Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
 100 105 110
 Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
 115 120 125
 Gly Ser Leu Gln Pro Leu Cys His Ser Asp Tyr Asp Glu Asp Asp Tyr
 130 135 140
 Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
 145 150 155 160
 Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
 165 170 175
 Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
 180 185 190
 Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
 195 200 205
 Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
 210 215 220
 Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
 225 230 235 240
 Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
 245 250 255
 Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
 260 265 270
 Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
 275 280 285
 Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
 290 295 300
 Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
 305 310 315 320
 Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
 325 330 335
 Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
 340 345 350
 Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
 355 360 365
 Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
 370 375 380
 Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
 385 390 395 400
 Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
 405 410 415
 Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
 420 425 430

Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
 435 440 445
 Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
 450 455 460
 Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
 465 470 475 480
 Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu
 485 490 495
 Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
 500 505 510
 Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
 515 520 525
 Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
 530 535 540
 Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
 545 550 555 560
 Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
 565 570 575
 Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His Ser
 580 585 590
 Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met Gly
 595 600 605
 Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
 610 615 620
 Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
 625 630 635 640
 Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
 645 650 655
 Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
 660 665 670
 Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
 675 680 685
 Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
 690 695 700
 Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
 705 710 715 720
 Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
 725 730 735
 Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
 740 745 750
 Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
 755 760 765
 Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln
 770 775 780
 Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
 785 790 795 800
 Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
 805 810 815
 Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
 820 825 830

Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
 835 840 845
 Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
 850 855 860
 Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
 865 870 875 880
 Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
 885 890 895
 Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
 900 905 910
 Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
 915 920 925
 Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
 930 935 940
 Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
 945 950 955 960
 Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
 965 970 975
 Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
 980 985 990
 Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
 995 1000 1005
 Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp Glu
 1010 1015 1020
 Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg Ser Gly
 1025 1030 1035 104
 Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe Ser Val Ala
 1045 1050 1055
 Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg Ile Phe Asp Leu
 1060 1065 1070
 Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu Ser Thr Asp Thr Asp
 1075 1080 1085
 Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu Glu Met Gly Lys Asn Ile
 1090 1095 1100
 Glu Asn Met Leu Gln Asn Lys Lys Thr Ser Ser Gln Leu Ser Arg Glu
 1105 1110 1115 112
 Arg Glu Glu Gln Glu Arg Lys Glu Leu Gln Arg Met Leu Leu Ala Ala
 1125 1130 1135
 Gly Ser Ala Ala Ser Gly Asn Asn His Arg Asp Asp Asp Thr Ala Ser
 1140 1145 1150
 Val Thr Ser Leu Asn Ser Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr
 1155 1160 1165
 Arg Thr Phe Arg Asp Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr
 1170 1175 1180
 Val Arg Lys Pro Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr
 1185 1190 1195 120
 Lys Asp Glu Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His
 1205 1210 1215
 Arg Glu Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg
 1220 1225 1230

Arg Leu

<210> 23
<211> 52
<212> DNA
<213> C. albicans

<400> 23
acgcgtcgac atgcatcatc atcatcatca tatggaggat ctaccaggg at 52

<210> 24
<211> 38
<212> DNA
<213> C. albicans

<400> 24
atagttagcg gccgcacact gctggtgtca accaacia 38

<210> 25
<211> 52
<212> DNA
<213> Human

<400> 25
acgcgtcgac atgcatcatc atcatcatca tatgggaccc ggctgcgatt tg 52

<210> 26
<211> 31
<212> DNA
<213> Human

<400> 26
gttgctctgc agctatcatg ctataataag c 31

<210> 27
<211> 31
<212> DNA
<213> Human

<400> 27
tgatagctgc agagcaacga ctgaaggatg c 31

<210> 28
<211> 32
<212> DNA
<213> Human

<400> 28
ccggtacctt cccgatgttg ttcataaaa ag 32

<210> 29
<211> 30
<212> DNA
<213> "Artificial Sequence"

<400> 29
acgcgtcgac atccaagttc aagttgtctg 30

<210> 30
<211> 42
<212> DNA
<213> "Artificial Sequence"

<400> 30
cgcggatccg cgctgcagtt ttcacatctt cttcttctgc ca 42

<210> 31
<211> 41
<212> DNA
<213> "Artificial Sequence"

<400> 31
aaaactgcag cgcggatccg cgtgcaggtg acgttattgg a 41

<210> 32
<211> 36
<212> DNA
<213> "Artificial Sequence"

<400> 32
atagtttagc ggccgccttg tgacaagaag tgacac 36

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